

IN THE CLAIMS:

Please amend claims 1, 4-10, 12, 16, 20, 23-25, 30, 34, 36-37, 40, 42-44, and 47-48. Cancel claims 11 and 35 as follows. For the Examiner's convenience, all pending claims are reproduced below. Applicant adds new claims 49-52.

a2 1 1 (Amended). A computer-implemented method of presenting expression level  
2 information as collected from first and second samples, said method comprising [the steps  
3 of]:  
4 displaying a first axis [corresponding to] indicating expression level in said  
5 first sample;  
6 displaying a second axis substantially perpendicular to said first axis, said  
7 second axis [corresponding to] indicating expression level in said second sample; [and]  
8 for a selected expressed sequence, displaying a mark at a position with an X  
9 coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative  
10 to said first axis and said Y coordinate of said position is selected relative to said second  
11 axis, wherein said position is selected relative to said first axis in accordance with an  
12 expression level of said selected expressed sequence in said first sample and relative to said  
13 second axis in accordance with an expression level of said selected expressed sequence in  
14 said second sample;  
15 receiving an input of a user's selection of said mark; and  
16 in response to said user input, displaying information about said selected  
17 expressed sequence.

1 2. The method of claim 1 wherein said selected expressed sequence  
2 comprises a gene.

1 3. The method of claim 1 wherein said selected expressed sequence  
2 comprises a portion of a gene.

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*28*

a3 1 4 (Amended). The method of claim 1 further comprising: [the step of]

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2 repeatedly [repeating said] displaying a mark [step] for each one of a plurality  
3 of selected expressed sequences.

1 5 (Amended). The method of claim 1 further comprising [the steps of]:  
2 monitoring said expression level of said expressed sequence in said first sample  
3 and said second sample.

1 6 (Amended). The method of claim [3] 5 wherein said monitoring [step for one  
2 of said samples] further comprises [substeps of]:

3 inputting a plurality of hybridization intensities [of] from pairs of perfect match  
4 and mismatch probes, said perfect match probes being perfectly complementary to a target  
5 nucleic acid sequence indicative of expression of said selected gene and said mismatch probes  
6 having at least one base mismatch with said target sequence, and said hybridization intensities  
7 indicating hybridization affinity between said perfect match and mismatch probes and a sample  
8 nucleic acid sequence from said one of said samples;

9 comparing the hybridization intensities of each pair of perfect match probe and  
10 mismatch probe; and

11 generating said expression level for said expressed sequence and said one of  
12 said samples responsive to results of said comparing [step].

1 7 (Amended). The method of claim 6 further comprising [the step of]:  
2 comparing a difference between hybridization intensities of perfect match and  
3 mismatch probes at a base position to a difference threshold.

1 8 (Amended). The method of claim 7 further comprising [the step of]:  
2 comparing a quotient of hybridization intensities of perfect match and mismatch  
3 probes at a base position to a ratio threshold.

1 9 (Amended). The method of claim 6 further comprising [the steps of]:  
2 a) counting a probe pair as a positive probe pair to increment a positive  
3 probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a

4 difference threshold and said perfect match probe intensity divided by said mismatch probe  
5 intensity exceeds a ratio threshold;

6 b) counting said probe pair as a negative probe pair to increment a  
7 negative probe pair count if said mismatch probe intensity minus said perfect match probe  
8 intensity exceeds said difference threshold and said mismatch probe intensity divided by said  
9 perfect match probe intensity exceeds said ratio threshold; **[and]**

10 c) computing a logarithmic ratio of said perfect match probe intensity to  
11 said mismatch probe intensity; and

12 d) computing a difference of said perfect match probe intensity to said  
13 mismatch probe intensity.

1 10 (Amended). The method of claim 9 further comprising **[the steps of]**:  
2 repeating said a), b), c) and **[c)] d)** steps for each of said probe pairs,  
3 accumulating a sum of differences of said perfect match and mismatch probe intensities for  
4 probe pairs that **[cause]** exhibit said difference; and  
5 determining an expression level of said selected expressed sequence to be an  
6 average of said differences.

1 11. Canceled.

2 11 ~~12~~ (Amended). The method of claim 1 ~~[11]~~ further comprising **[the steps**  
3 **of]**:  
4 in response to said **[user]** input, displaying information about said selected  
5 expressed sequence; said information comprising an identifier for said selected expressed  
6 sequence.

1 12 ~~13~~ (Amended). The method of claim 11 ~~12~~ wherein said **[information**  
2 **about]** identifier for said selected expressed sequence comprises a GenBank accession  
3 number.

1 14. The method of claim 12 wherein said information about said selected  
2 expressed sequence comprises a GenBank database record for said selected expressed  
3 sequence.

1 15. The method of claim 1 wherein said first sample and said second  
2 sample are collected from tissue samples differing in a particular characteristic.

95 1 15 ~~18~~ (Amended). The method of claim ~~15~~<sup>14</sup> wherein said particular  
2 characteristic comprises [**presence of**] a disease state.

1 17. The method of claim 15 wherein said particular characteristic comprises  
2 a treatment strategy for a disease.

1 18. The method of claim 1 wherein said particular characteristic is a stage of  
2 a disease.

96 1 18 ~~19~~ (Amended). The method of claim 1 further comprising [**the step of**]:  
2 displaying a third axis substantially perpendicular to said first axis and to said  
3 second axis in a three-dimensional display environment wherein said position of said mark is  
4 further selected relative to said third axis in accordance with an expression level of said  
5 selected expressed sequence in a third sample.

96 1 19 ~~20~~ (Amended). A computer-implemented method of presenting sample  
2 analysis information comprising [**the steps of**]:

3 displaying a first axis [**corresponding to**] indicating a concentration of a  
4 compound in a first sample as determined by monitoring binding of said compound to a  
5 selected polymer having binding affinity to said compound;

6 displaying a second axis substantially perpendicular to said first axis, said  
7 second axis [**corresponding to**] indicating a concentration of said compound in said second  
8 sample as determined by monitoring binding of said compound to said selected polymer; and

9 displaying a mark at a position with an X coordinate and a Y coordinate,  
10 wherein the X coordinate of said position is selected relative to said first axis and said Y

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11 coordinate of said position is selected relative to said second axis, wherein said position is  
12 selected relative to said first axis in accordance with said concentration in said first sample and  
13 relative to said second axis in accordance with said concentration in said second sample;  
14 receiving an input of a user's selection of said mark; and  
15 in response to said user input, displaying information about said <sup>compound</sup> ~~selected~~  
16 expressed sequence.

1 21. The method of claim 20 wherein said selected polymer comprises a  
2 nucleic acid sequence.

1 22. The method of claim 20 wherein said selected polymer comprises a  
2 protein.

1 22 ~~23~~ (Amended). The method of claim ~~21~~<sup>20</sup> further comprising [the step of]:  
2 obtaining said concentration of said compound in said first sample by exposing  
3 said first sample to a plurality of nucleic acid probes.

1 23 ~~24~~ (Amended). The method of claim ~~21~~<sup>21</sup> further comprising [the step of]:  
2 obtaining said concentration of said compound in said first sample by exposing  
3 said first sample to a plurality of peptide probes.

1 24 ~~25~~ (Amended). A computer program product for presenting expression  
2 level information as collected from a first sample and a second [samples] sample, said product  
3 comprising:[:]  
4 code for displaying a first axis [corresponding to] indicating expression level  
5 in said first sample;  
6 code for displaying a second axis substantially perpendicular to said first axis,  
7 said second axis [corresponding to] indicating expression level in said second sample;  
8 code for, for a selected expressed sequence, displaying a mark at a position with  
9 an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected  
10 relative to said first axis and said Y coordinate of said position is selected relative to said  
11 second axis, wherein said position is selected relative to said first axis in accordance with an

12 expression level of said selected expressed sequence in said first sample and relative to said  
13 second axis in accordance with an expression level of said selected expressed sequence in said  
14 second sample;

15 code for receiving an input from a user's selection of said mark;  
16 code for displaying information about said selected expressed sequence in  
17 response to said user input; and  
18 a computer-readable storage medium for storing the codes.

1 26. The product of claim 25 wherein said selected expressed sequence  
2 comprises a gene.

1 27. The product of claim 25 wherein said selected expressed sequence  
2 comprises a portion of a gene.

1 28. The product of claim 25 further comprising code for repeatedly applying  
2 said displaying a mark code for a plurality of selected expressed sequences.

1 29. The product of claim 25 further comprising:  
2 code for monitoring said expression level of said expressed sequence in said  
3 first sample and said second sample.

1 2A 30 (Amended). The product of claim <sup>25</sup>[27] ~~26~~ wherein said code for  
2 monitoring [step] for one of said samples comprises:

3 code for inputting a plurality of hybridization intensities [of] from pairs of  
4 perfect match and mismatch probes, said perfect match probes being perfectly complementary  
5 to a target nucleic acid sequence indicative of expression of said selected gene and said  
6 mismatch probes having at least one base mismatch with said target sequence, and said  
7 hybridization intensities indicating hybridization affinity between said perfect match and  
8 mismatch probes and a sample nucleic acid sequence from said one of said samples;  
9 code for comparing the hybridization intensities of each pair of perfect match  
10 probe and mismatch probe; and

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11 code for generating said expression level for said expressed sequence and said  
12 one of said samples responsive to a result produced by [results of] said code for comparing  
13 [step].

1 31. The product of claim 30 further comprising:  
2 code for comparing a difference between hybridization intensities of perfect  
3 match and mismatch probes at a base position to a difference threshold.

1 32. The product of claim 31 further comprising:  
2 code for comparing a quotient of hybridization intensities of perfect match and  
3 mismatch probes at a base position to a ratio threshold.

1 33. The product of claim 30 further comprising:  
2 a) code for counting a probe pair as a positive probe pair to increment a positive  
3 probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a  
4 difference threshold and said perfect match probe intensity divided by said mismatch probe  
5 intensity exceeds a ratio threshold;

6 b) code for counting said probe pair as a negative probe pair to increment a  
7 negative probe pair count if said mismatch probe intensity minus said perfect match probe  
8 intensity exceeds said difference threshold and said mismatch probe intensity divided by said  
9 perfect match probe intensity exceeds said ratio threshold; and

10 c) code for computing a logarithmic ratio of said perfect match probe intensity  
11 to said mismatch probe intensity.

1 33 34 (Amended). The product of claim <sup>32</sup>33 further comprising:  
2 code for repeatedly applying said a), b), and c) codes for each of said probe  
3 pairs, accumulating a sum of differences of said perfect match and mismatch probe intensities  
4 for probe pairs that [cause] exhibit said difference; and  
5 code for determining an expression level of said selected expressed sequence to  
6 be an average of said differences.

1 35. Canceled.

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1 34 36 (Amended). The product of claim [35] 24 further comprising:  
2 code for, in response to said [user] input, displaying information about said  
3 selected expressed sequence; said information comprising an identifier for said selected  
4 expressed sequence.

1 35 37 (Amended). The product of claim 34 wherein said [information  
2 about] identifier for said selected expressed sequence comprises a GenBank accession number.

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1 38. The product of claim 36 wherein said information about said selected  
2 expressed sequence comprises a GenBank database record for said selected expressed  
3 sequence.

1 39. The product of claim 25 wherein said first sample and said second  
2 sample are collected from tissue samples differing in a particular characteristic.

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1 38 40 (Amended). The product of claim 37 wherein said particular  
2 characteristic comprises [presence of] a disease state.

1 41. The product of claim 39 wherein said particular characteristic comprises  
2 a treatment strategy for a disease.

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1 40 42 (Amended). The product of claim [25] 37 wherein said particular  
2 characteristic is a stage of a disease.

1 41 43 (Amended). The product of claim 24 further comprising [the step of] :  
2 code for displaying a third axis substantially perpendicular to said first axis and  
3 to said second axis in a three-dimensional display environment wherein said position of said  
4 mark is further selected relative to said third axis in accordance with an expression level of said  
5 selected expressed sequence in a third sample.

1 42 44. A computer program product for presenting sample analysis information  
2 comprising:

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code for displaying a first axis **[corresponding to]** indicating a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having bonding affinity to said compound;

code for displaying a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating a concentration of said compound in a second sample as determined by monitoring binding of said compound to said selected polymer;

code for displaying a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample;

**[and]**

code for receiving an input of a user's selection of said mark;

code for displaying information about said <sup>compound</sup> selected expressed sequence in response to said user input; and

a computer-readable storage medium that stores the codes.

45. The product of claim 44 wherein said selected polymer comprises a nucleic acid sequence.

46. The product of claim 44 wherein said selected polymer comprises a protein.

45 47 (Amended). A computer system comprising a display, a processor, and a memory that stores instructions for configuring said processor to:

display a first axis **[corresponding to]** indicating expression level in said first sample;

display a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating expression level in said second sample; and

for a selected expressed sequence, display a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to

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conclude

9 said first axis and said Y coordinate of said position is selected relative to said second axis,  
10 wherein said position is selected relative to said first axis in accordance with an expression  
11 level of said selected expressed sequence in said first sample and relative to said second axis in  
12 accordance with an expression level of said selected expressed sequence in said second  
13 sample; wherein information about said selected expressed sequence is displayed responsive to  
14 an input of a user's selection of said mark.

46 48 (Amended). A computer system comprising a display, a processor,  
2 and a memory that stores instructions for configuring said processor to:

3 display a first axis [**corresponding to**] indicating a concentration of a  
4 compound in a first sample as determined by monitoring binding of said compound to a  
5 selected polymer having binding affinity to said compound;

6 display a second axis substantially perpendicular to said first axis, said second  
7 axis [**corresponding to**] indicating a concentration of said compound in said second sample as  
8 determined by monitoring binding of said compound to said selected polymer; and

9 display a mark at a position with an X coordinate and a Y coordinate, wherein  
10 the X coordinate of said position is selected relative to said first axis and said Y coordinate of  
11 said position is selected relative to said second axis, wherein said position is selected relative to  
12 said first axis in accordance with said concentration in said first sample and relative to said  
13 second axis in accordance with said concentration in said second sample; wherein information  
14 about said selected expressed sequence is displayed responsive to an input of a user's selection  
15 of said mark.

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1 47 49 (New) The method of claim 1 further comprising:  
2 providing a tactile feedback to said user through a pointing device when a  
3 cursor is moved over said mark; said tactile feedback indicating expression level for said  
4 selected expressed sequence corresponding to said mark.

1 48 50 (New) The method of claim 1 further comprising:

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2 providing an aural indication to said user through a pointing device when a  
3 cursor is moved over said mark; said aural indication indicating expression level for said  
4 selected expressed sequence corresponding to said mark.

1 49 ~~51~~. (New) The method of claim 1 further comprising:  
2 obtaining information from an internet based resource about a selected  
3 expressed sequence corresponding to said mark.

2 50 ~~52~~. (New) The method of claim 1 further comprising:  
3 receiving from the user a selection of at least two of a plurality of marks, said  
4 marks;  
5 displaying information about genes corresponding to said selection of at least  
two of a plurality of marks.

REMARKS

REJECTIONS UNDER 35 U.S.C. § 112(2)

Applicant amends the claims to avoid the Examiner's 35 U.S.C. 112 rejections in paragraphs A-P. No amendment should be construed as acquiescence in any grounds of rejection.

Regarding the Examiner's rejection in paragraph A, applicant notes that the axes that define a coordinate system meet at a point called the "origin" and are thus connected. However, applicant notes that not all embodiments according to the present invention need necessarily display the origin, or connection point, of the axes. Applicant believes the issue is not one of indefiniteness, but rather one of scope, and has therefore not changed the claims.

Regarding the Examiner's rejection in paragraph N, applicant notes the specification describes the treatment strategy as a characteristic on page 12, lines 22-25:

One can compare expression levels among tissue samples at successive stages or severity levels of the same disease, among tissue samples where different ultimate outcomes of the disease (e.g., patient death or